UNITED STATES PATENT AND TRADEMARK OFFICE

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ART UNIT	PAPER NUMBER
1631	

DATE MAILED: 01/21/2005

Please find below and/or attached an Office communication concerning this application or proceeding.

PTO-90C (Rev. 10/03)

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE _3_ MONTH(S) FROM
THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed
  after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
  Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any
  earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on _01 November 2004_.

2a)☒ This action is **FINAL**.   2b)☐ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is
closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) _1-23_ is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) _1-23_ is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☒ Claim(s) _1-23_ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All   b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage
application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1)☐ Notice of References Cited (PTO-892)
2)☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3)☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08)
Paper No(s)/Mail Date _1 page_.

4)☐ Interview Summary (PTO-413)
Paper No(s)/Mail Date. _____.
5)☐ Notice of Informal Patent Application (PTO-152)
6)☐ Other: _____.

DETAILED ACTION

Applicants' remarks, filed 11/1/04, are acknowledged.

Applicants' arguments, filed 11/1/04, have been fully considered but they are not deemed

to be persuasive. Rejections and/or objections not reiterated from the previous office actions are

hereby withdrawn. The following rejections and/or objections are either reiterated or newly

applied. They constitute the complete set presently being applied to the instant application.

The information disclosure statement filed 11/1/04 fails to comply with the provisions of

37 CFR 1.97, 1.98, and MPEP § 609, because reference "BLAST Help Manual" lacks a

publication date. It has been placed in the application file, but the information referred to therein

has not been considered as to the merits. Applicant is advised that the date of any re-submission

of any item of information contained in this information disclosure statement or the submission

of any missing element(s) will be the date of submission for purposes of determining compliance

with the requirements based on the time of filing the statement, including all certification

requirements for statements under 37 CFR 1.97(e). See MPEP § 609, ¶ C(1).

Claims 1-23 are herein under examination.

Claims Rejected Under 35 U.S.C. § 112, Second Paragraph

The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

The rejection of claims 1-23 is maintained under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which the applicant regards as the invention.

The rejections are maintained and reiterated for reasons of record.

Applicants make reference to MPEP § 2173.01 that Applicants are their own lexicographers and may use functional language as long as the boundaries of the subject matter in the claims are clear. It is true Applicants can be their own lexicographers and should state claims clearly so that the metes and bounds of the claims is understood. It is acknowledged that Applicants make reference to MPEP § 2173.02 which suggests how an Examiner should examine 35 U.S.C. 112, second paragraph, issues. Applicants state that the essential inquiry pertaining to this requirement is whether the claims set out and circumscribe a particular subject matter with a reasonable degree of clarity and particularity. This statement is acknowledged. Applicants state the term "efficient" might raise concerns in regard to MPEP 2173.05(b) as possible relative terminology, and they suggest it is a descriptive term. This statement is found unpersuasive as this is a term that lacks clarity. Applicants state the term "efficient" has an understood meaning in the art and the specification provides standards, in the form of examples, that would apprise one of skill in the art as to the claim scope. This statement is found unpersuasive as examples do not form an explicit definition including metes and bounds of this

term. Applicants state the breadth of a claim is not to be equated with indefiniteness. This statement is acknowledged; however, not knowing intended metes and bounds of a term renders a lack of clarity in the term. The phrases rejected below under 35 U.S.C. 112, second paragraph, do not fall into the realm of having a reasonable degree of clarity and particularity for the reasons given below.

Claims 4 (line 4) and claim 16 (line 4), recite the phrase "efficient structure" which is vague and indefinite. It is unclear what criteria or to what degree one considers the structure to be efficient. For example, one definition of "efficient" on the online Merriam-Webster's dictionary is "productive of desired effects". Therefore, one of skill in the art would question what characteristics must be present for the structure to contain these desired effects. Clarification of the metes and bounds of this phrase via clearer claim wording is requested. Applicants state they previously presented examples in the specification of an "efficient structure" in the field of bioinformatics. This statement is found unpersuasive as examples do not provide an explicit definition of the intended meaning of the phrase. Applicants state it is inappropriate to use a Merriam-Webster definition of "efficient". This statement is found unpersuasive because when there is no explicit definition of a term in the specification, the Examiner is required to examine the term in a broad and reasonable sense that includes dictionary definitions. Applicants make reference to a sentence in a Matsumoto et al. reference. This reference states the "most efficient way" which is yet another example; however, it remains unclear if Applicants are talking about the most efficient way, a semi-efficient way, or any other part along the spectrum of efficiency without a clarification of the metes and bounds of the

phrase. Providing examples does not clarify the metes and bounds of the phrase "efficient structure".

Applicants direct the Examiner to paragraph 68 which they say defines "efficient structure" as "efficient structure, e.g. 2 bits per nucleotide with appropriate encoding, 5 bits per amino acid residue with appropriate encoding, etc.". This is statement is found unpersuasive as this "e.g." is an example, rather than a definition that gives clear metes and bounds of the phrase. Applicants state the phrase is not indefinite, but broad. This is found unpersuasive as there are certain elements to this phrase, as discussed above, that lead one of skill not to know how to clearly interpret the metes and bounds of the phrase. Applicants give examples of efficient structure, but these examples rely on one structure being compared to another, such that some type of reference is given to adequately support how the efficiency is perceived. However, the phrase "efficient structure" alone in the claim without such reference to what or how it is more efficient, results in one of skill in the art not knowing how to determine if the structure is in fact efficient.

Claims 7 (line 5) and 19 (line 6), recite the word "efficiently encoded representation of alignment" which is vague and indefinite. It is unclear what criteria or to what degree one considers the representation of alignment to be efficiently encoded. For example, one definition of "efficient" on the online Merriam-Webster's dictionary is "productive of desired effects". Therefore, one of skill in the art would question what characteristics must be present for the encoded representation of alignment to contain these desired effects. Clarification of the metes and bounds of this phrase via clearer claim wording is requested. Claims 8-11 and 20-22 are also rejected due to their direct or indirect dependence from claims 7 and 19.

Applicants submit that one of skill in the art would clearly understand the meaning of the above-mentioned phrase. This statement is found unpersuasive as the phrase including the term "efficiently" renders the claim unclear to one of ordinary skill in the art due to the unclarity of the metes and bounds of the word, phrase, and therefore claim. Applicants suggest that the efficient coding entails use of the minimum number of bits needed to represent the data. Applicants state that paragraph 19 uses efficient coding. This statement is found unpersuasive as paragraph 19 appears to be another example that does not explicitly define the rejected phrase. Applicants make reference to a sentence in a Matsumoto et al. reference. This reference states the "most efficient way" which is yet another example; however, it remains unclear if Applicants are talking about the most efficient way, a semi-efficient way, or any other part along the spectrum of efficiency without a clarification of the metes and bounds of the phrase. Providing examples does not clarify the metes and bounds of the phrase "efficient structure". Applicants refer to a Varre et al. reference stating "efficient encoding procedures are known." One reference does not render something well known in the art. These extra references do not satisfy the lack of clarity regarding the metes and bounds of these rejected phrases due to the mere use of examples.

Claim 8, lines 1-2, recites the phrase "seed point and sum-set membership" which is vague and indefinite. It is unclear how the Applicants intend this phrase to be defined. Clarification of the meaning of this phrase is requested.

Applicants state that one of skill in the art would readily understand the definitions of the terms "seed" (a matching word/string) and "sum" (a part of the scoring when using BLAST) (page 7, third paragraph of Response). This statement is not supported (via documentation) to

provide sound evidence that these terms are well-known in the art. In fact, these terms could

have various meanings in the field of bioinformatics and mathematics. Applicants' statement is

found unpersuasive as "Basic Local Alignment Search Tool" by Altschul et al. (1990; see prior

art reference in 35 U.S.C. § 103 rejection in previous Office Action, mailed 2/13/03) is an article

that describes BLAST in detail, but makes no mention of these particular terms. Applicants

attempt to define "seed point and sum-set membership" by using various interpretations set forth

in various articles. These statements appear to be interpretations or examples that are not

necessarily considered to be well known in the art. A reference to a phrase in a published article

does not automatically equate it to being well known in the art and thus understood by one

skilled in the art. On page 7, first full paragraph of Applicants' remarks, Applicants state how

they interpret "seed point and sum-set membership". This interpretation appears to add many

limitations which are not apparent in the simple use of the rejected phrase. Providing examples

does not clarify the metes and bounds of the phrase.

Claims 1 (line 16) and 13 (line 22) recite the phrase "said task definition" which is

rejected due to the lack of clear antecedent basis. Several task definitions are mentioned

previously in these claims so it is unclear to which one this phrase is referring. Claims 2-12 and

14-23 are also rejected due to their direct or indirect dependency from claims 1 and 23.

Applicants state the use of singular "said task definition" limits the antecedent basis to

the prior singular limitation "sending a task definition for each task from the master CPU to one

of a plurality of slave CPUs" (claim 1) and "sending a task definition for each task to one of a

plurality of slave CPUs" (claim 13). This statement is found unpersuasive various task

definitions are previously mentioned, including claim 1 (lines 8, 9, and 13-15) and claim 13

(lines 12, 14, 19, and 20).

Claim Rejections – 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all

obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth
> in section 102 of this title, if the differences between the subject matter sought to be patented and the prior
> art are such that the subject matter as a whole would have been obvious at the time the invention was made
> to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be
> negatived by the manner in which the invention was made.

This application currently names joint inventors. In considering patentability of the

claims under 35 U.S.C. 103(a), the examiner presumes the subject matter of the various claims

was commonly owned at the time any inventions covered therein were made absent any evidence

to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point the inventor

and invention dates of each claim that was not commonly owned at the time a later invention was

made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35

U.S.C. (e), (f) or (g) prior art under 35 U.S.C. 103(a).

The rejection of claims 1, 4, 6-13, and 18-23 is maintained under 35 U.S.C. 103(a) as

being unpatentable over Smith et al. (Genome Research, 1996, Volume 6, pages 454-462) in

view of Altschul et al. (Journal of Molecular Biology, 1990, Volume 215(3), pages 403-410 and

Reed et al. (P/N 5,862,325).

The rejection is maintained and reiterated for reasons of record.

Smith et al. describe an integrated set of World Wide Web pages that organize nucleic

acid sequence searches and analyses available by function and provide a single entry for related

searches (abstract) which represents a "system" which is defined by the online Merriam-Webster

dictionary as an integrating group of items forming a unified whole as well as an organization

forming a network especially for distributing something serving a common purpose. This system

provides a method of performing different searches for a given query sequence (query dataset N)

with various sequence databases (i.e. BLAST database which represents subject dataset M)

(abstract; page 455, col. 2, first paragraph; and page 457, col. 2, first paragraph) which represents

a method of comparing datasets. Smith et al. describe nucleic acid sequence search services,

involving genomic databases in Table 1, as stated in instant claims 12 and 23. Smith et al.

describe a sequence input field which for nucleic acid searches (page 455, col. 1, third paragraph

to col. 2, first paragraph) which is well known in the art to be divided into nucleotides (data

elements). The presence of an input field suggests that there is a size limitation with a specified

range, such as being more than zero but less than infinity. Smith et al. describe BLAST nucleic

acid sequence searches in Table 1, including a dbEST DB. This EST (Expressed Sequence Tag)

database subset represents a division of the BLAST database (subject dataset) which has a size

within a specified range, as stated in instant claims 1 and 13, since EST is defined online

Genome Glossary as a short (size) strand of DNA that is part of a cDNA molecule. Smith et al.

describe using the Internet allowing for communication between remote sites and promoting a

distributed information space by filling out a HTML form (user input query) on a web page (at a

master CPU (central processing unit)), launching a search at a remote site (slave CPU), returning

results for further processing by the BCM Search Launcher server (another slave CPU), and

presenting results to the user (from original master CPU) (page 459, col. 2, third paragraph). As

the master-slave is defined by online Webopedia as "an architecture in which one device

(master) controls one or more other devices (the slaves), the description provided in the sentence

above represents sending information to a master CPU of a master-slave distributed computing

platform (via query input) by sending data elements referenced by a task definition to said slave

CPU, performing each task (i.e. comparison search and further processing) on a slave CPU and

returning task results for each task to said master CPU. Smith et al. describe using a plurality of

servers (slave CPUs) that can return results to the user's system (master CPU) with additional

links to auxiliary information that was initiated from a single entry page (abstract and page 455,

col. 1, third paragraph). Smith et al. describe user (at master CPU) selecting task definitions

such as specified search parameters, choosing a search server (an executable element capable of

performing comparisons) with a form tag, selecting a function type to submit the form containing

user input (all available data elements and task definitions) to an external program (an executable,

element capable of performing comparisons), and sequence name/identifier (query and subject

data element identification/descriptor) (page 459, col. 2, third paragraph to page 460, col. 1, third

paragraph). Smith et al. describe being able to specify one or more query parameter values (page

460, col. 1, fourth paragraph) which represents more than one data element dataset that can be

query or subject in nature, as the term "subject" is a very broad term. Smith et al. describe

generating a BLAST report for each query data element as seen in Figure 2 (3). Smith et al.

describe concatenating results (page 454, col. 2, first paragraph and page 457, col. 2, first

paragraph) from all BLAST reports (page 461, col. 1, second paragraph) to produce a text file

identical to blastall run of query and subject datasets as seen in Figure 2 and Figure 2 caption

(page 459), as stated in instant claims 10, 11, 21, and 22. Smith et al. describe storing seed point

and sum-set membership of each alignment in BLAST as seen in Figure 2 (third window from

top on left side), as stated in instant claim 8. Smith et al. describe storing results from tasks into

results files including query and subject sequence data and metadata corresponding to the task

that the results came from, links to sequences that are similar to sequence matched in database

search (metadata for the subject sequence) (page 455, col.2 , last paragraph to page 456, col. 1

and 2), partial subject sequence data corresponding to the subject bounds of the significant

alignment result, and other results data (see Figure 2), as stated in instant claims 9 and 20. Smith

et al. describe a list (index) of information about query and subject sequence (i.e. third and fourth

windows from top left as well bottom right window in Figure 2), including bounds information

for start and stop of subsequences (i.e. third window from top left of Figure 2), storing data

including hits, scores, identities, and positives (data quantifying fulfillment of significance

criteria for a significant match (i.e. third window from top left of Figure 2), and storing an

efficiently encoded representation of alignment between said bounds corresponding to a high

scoring pair (see alignment in third window from top left of Figure 2), as stated in instant claims

7 and 19. Smith et al. do not describe compressing and uncompressing data as well as looping

processes.

Altschul et al. describe compressing the database by packing 4 nucleotides into a single

byte and using a table to delimit the boundaries between adjacent sequences (page 405, col. 1,

lines 37-40). Altschul et al. describe beginning with a matrix of similarity scores for all possible

pairs of residues (page 404, col. 1, paragraph 3) which represents determining the number of

tasks for an entire comparison of two datasets. Altschul et al. describe performing BLAST with

two random sequences (data sets N and M) of lengths m and n in order to determine the

probability of finding a segment pair with a score greater than S (cut off score, page 404, col. 2,

second paragraph) where $y = Kmn\, e^{-\lambda S}$ (page 405, col. 2, equation 1 and fourth paragraph) which

represents determination of a number of tasks or points in a matrix in a comparison of two

datasets (i.e. N and M) involving a multiplication of data elements $n_N \times n_M$, as stated in instant

claims 1 and 13. Altschul et al. describe the sequence segments can be of any length (page 404,

col. 1, lines 34-36) or certain short sequences thus having a specified range (page 404, col. 2,

lines 61-63). Altschul et al. use a list, or index, of all 12-mers in a query sequence in one

example (page 405, col. 1, lines 33-35).

Reed et al. describe a system and methods that coordinate the transfer of data, metadata,

and instructions between databases to control and process communications (abstract and col. 1,

lines 10-14) which represents a separation or stripping of metadata from data. Reed et al.

describe this transfer of metadata and methods allow for the control by the provider and

consumer of the types and contents of information subsequently transferred (abstract) which

represents storing minimal information if so desired. Reed et al. describe compressing database,

database query, or other file format using PKZIP (col. 14, lines 41-47 and col. 53, line 1) that

represents packing data into an efficient structure using a redundancy reduction data compression

method. Reed et al. describe corresponding data, metadata, and instructions in the provider

program can control and automate decryption and decompression of data (col. 14, lines 47-51).

Reed et al. describe communication networks that allow both parties to control, filter, store,

index, and process communications from each other (col. 7, lines 63 to col. 8, line 2) which

represents creating an index in an uncompressed manner. Reed et al. describe querying a

provider database and loops through each communication object instance (data) which is to be

published and which are read (col. 32, lines 28-35) which represents a looping of data (i.e. query

sequences) to perform setup, preprocessing, and table generation. Reed et al. describe the

program begins a second loop through each recipient and using such recipient attributes and

methods to generate and transmit a communications object instance for all recipients (col. 32,

lines 35-42) which represents a looping of other data such as the looping of subject sequences.

Smith et al. state sequence analysis services are extremely useful for molecular biologists

to allow access to the ever-expanding sequence data bases without requiring copious local data

base storage, frequent data base updates, the cost of expensive and sophisticated hardware and

software, and the cost and effort of continuous system maintenance (page 454, col. 1, first

paragraph). Smith et al. state that the individual WWW server sites scattered throughout the

Web hinders their efficient use (page 455, col. 1, first paragraph). Smith et al. state the BCM

Search Launcher addresses these limitations by providing an improved interface to simplify

access and improve analysis resources (page 455, col. 1, second paragraph). A skilled artisan in

the art would have been motivated to make improvements to analysis server sites, such as that

stated by Smith et al. (page 455, col. 1, first paragraph) additional features to further simplify

access and improve analysis resources (page 455, col. 1, second paragraph). Therefore, it would

have been obvious to one having ordinary skill in the art at the time the invention was made to

compress data (as stated by Altschul et al. and Reed et al.) and looping processes (as stated by

Reed et al.) in order to offer enhanced, integrated, easy-to-use, and time-saving techniques to a

large number of useful molecular biology database search and analysis services for organizing

and improving access to these tools for genome researchers worldwide (Smith et al., page 459,

col. 1, third paragraph to col. 2, first paragraph).

Thus, Smith et al. in view of Altschul et al. and Reed et al. motivate the limitations in

claims 1, 4, 6-13, and 18-23.

Applicants state that there is no motivation or suggestion to combine references. This

statement is found unpersuasive as Smith et al. state the problem of hindering efficient use as

well as improving and simplifying access and sources which is a proper motivation to combine.

Applicants state the references do not mention distributed computing. This is found

unpersuasive as the instant claims do not recite the phrase "distributed computing", but rather a

CPU of a master-slave distributed computing platform (i.e. claim 1, lines 7-8). The "system"

definition can be interpreted to represent such a platform in the Smith et al. reference.

Applicants state that one should look to the broadest reasonable interpretation consistent with the

specification as required by MPEP 2111. It is noted that limitations in the specification are not

to be automatically applied to the claim limitations and a broad and reasonable interpretation is

acceptable especially when Applicants fail to provide an explicit definition of term or phrase

used in the recited claims. Applicants state Smith et al. teach away from the instant invention in

teaching serial use as opposed to in parallel use at multiple slave CPUs. This statement is found

unpersuasive as the instant claims do not recite in parallel use in their limitations. Applicants

state Altschul et al. teach away from the instant invention by teaching dataset-to-dataset

comparison on a single machine. It is noted that not all of the limitations need to be found in

each reference, but rather need to be found in one of the combination of references which is why

this is a 35 USC 103 rejection and not a 35 USC 102 rejection. Applicants state the Reed et al.

reference borders on the ridiculous with nothing to do with bioinformatics or dataset

comparisons. This is found unpersuasive as the Reed et al. reference deals with computer data,

an essential component of bioinformatics. Applicants state the compression in col. 57 of Reed et

al. is for word processing documents like PKZIP, not databases. It is noted that Reed et al.

disclose compressing databases in col. 14, lines 41-47. Additional reference was made in col.

53, not col. 57. Other compression algorithms preferred by the provider may be used (i.e. SIT)

or the next most preferred format (as stated in col. 52, line 67 to col. 53, lines 1-6). Applicants

state the motivation to combine references is completely unrelated to the claim limitations. It is

not agreed that the motivation is completely unrelated to the claim limitations, but it is also noted

that the reasons to combine references need not be the same motivations for the instant invention.

Applicants state one of ordinary skill in the art could not reasonably expect to find the

Applicants' invention for comparing large datasets or processing them in parallel over a network

with the cited prior art. This is found unpersuasive as the instant claims do not state large

datasets or in parallel processing. Applicants state that various limitations, namely those listed in

instant claim 1, are not described by Smith et al. This statement is found unpersuasive as the 35

USC 103 rejection stated above mentions every limitation as found in the prior art references.

Limitations not described by Smith et al. are described by the other two references. Applicants

state Smith et al.'s selection of a sequence to "clip and paste" into the HTML input form is not a

division of a query dataset N, no datasets are divided, no tasks are determined, and no elements

are sent to a master CPU. These statements are found unpersuasive as the limitations are found

in the passage stated below:

Smith et al. describe a sequence input field which for nucleic acid searches (page 455, col. 1, third paragraph to col. 2, first paragraph) which is well known in the art to be divided into nucleotides (data elements). The presence of an input field suggests that there is a size limitation with a specified range, such as being more than zero but less than infinity. Smith et al. describe BLAST nucleic acid sequence searches in Table 1, including a dbEST DB. This EST (Expressed Sequence Tag) database subset represents a division of the BLAST database (subject dataset) which has a size within a specified range, as stated in instant claims 1 and 13, since EST is defined online Genome Glossary as a short (size) strand of DNA that is part of a cDNA molecule. Smith et al. describe using the Internet allowing for communication between remote sites and promoting a distributed information space by filling out a HTML form (user input query) on a web page (at a master CPU (central processing unit)), launching a search at a remote site (slave CPU), returning results for further processing by the BCM Search Launcher server (another slave CPU), and presenting results to the user (from original master CPU) (page 459, col. 2, third paragraph). As the master-slave is defined by online Webopedia as "an architecture in which one device (master) controls one or more other devices (the slaves), the description provided in the sentence above represents sending information to a master CPU of a master-slave distributed computing platform (via query input) by sending data elements referenced by a task definition to said slave CPU, performing each task (i.e. comparison search and further processing) on a slave CPU and returning task results for each task to said master CPU. Smith et al. describe using a plurality of servers (slave CPUs) that can return results to the user's system (master CPU) with additional links to auxiliary information that was initiated from a single entry page (abstract and page 455, col. 1, third paragraph). Smith et al. describe user (at master CPU) selecting task definitions such as specified search parameters, choosing a search server (an executable element capable of performing comparisons) with a form tag, selecting a function type to submit the form containing user input (all available data elements and task definitions) to an external program (an executable element capable of performing comparisons), and sequence name/identifier (query and subject data element identification/descriptor) (page 459, col. 2, third paragraph to page 460, col. 1, third paragraph). Smith et al. describe being able to specify one or more query parameter values (page 460, col. 1, fourth paragraph) which represents more than one data element dataset that can be query or subject in nature, as the term "subject" is a very broad term.

Applicants state the other references fail to disclose any of the limitations missing by Smith et al. This statement is found unpersuasive as all of the references combined describe the claimed invention as detailed in the rejection above. Applicants' arguments are deemed unpersuasive such that the 35 USC 103 rejection is maintained.

Conclusion

No claim is allowed.

THIS ACTION IS MADE FINAL. Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the mailing date of this final action.

Papers related to this application may be submitted to Technical Center 1600 by facsimile transmission. Papers should be faxed to Technical Center 1600 via the PTO Fax Center. The faxing of such papers must conform with the notices published in the Official Gazette, 1096 OG 30 (November 15, 1988), 1156 OG 61 (November 16, 1993), and 1157 OG 94 (December 28, 1993) (See 37 CFR §1.6(d)). The Central Fax Center number for official correspondence is (571) 273-8300.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Carolyn Smith, whose telephone number is (571) 272-0721. The examiner can normally be reached Monday through Thursday from 8 A.M. to 6:30 P.M.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's

supervisor, Ardin Marschel, can be reached on (571) 272-0718.

Any inquiry of a general nature or relating to the status of this application should be

directed to Legal Instruments Examiner Tina Plunkett whose telephone number is (571) 272-

0549.

January 11, 2005

ARDIN H. MARSCHEL
PRIMARY EXAMINER